Figure S1. Sample clustering to detect outliers based on mRNA data in weighted gene co-expression network analysis.

Sample clustering to detect outliers

Figure S2. Weighted gene co-expression network analysis. (A) Sample dendrogram and trait heatmap based on gene expression data. (B and C) Analysis of scale-free fit index and the mean connectivity for various soft-thresholding powers. Scale-free topology was tested when β=7. (D) Clustering dendrograms of genes, with dissimilarity based on topological overlap, together with assigned module colors. (E) The heatmap depicts the topological overlap matrix amongst genes based on co-expression modules. A higher degree of module correlation is indicated by a darker background.
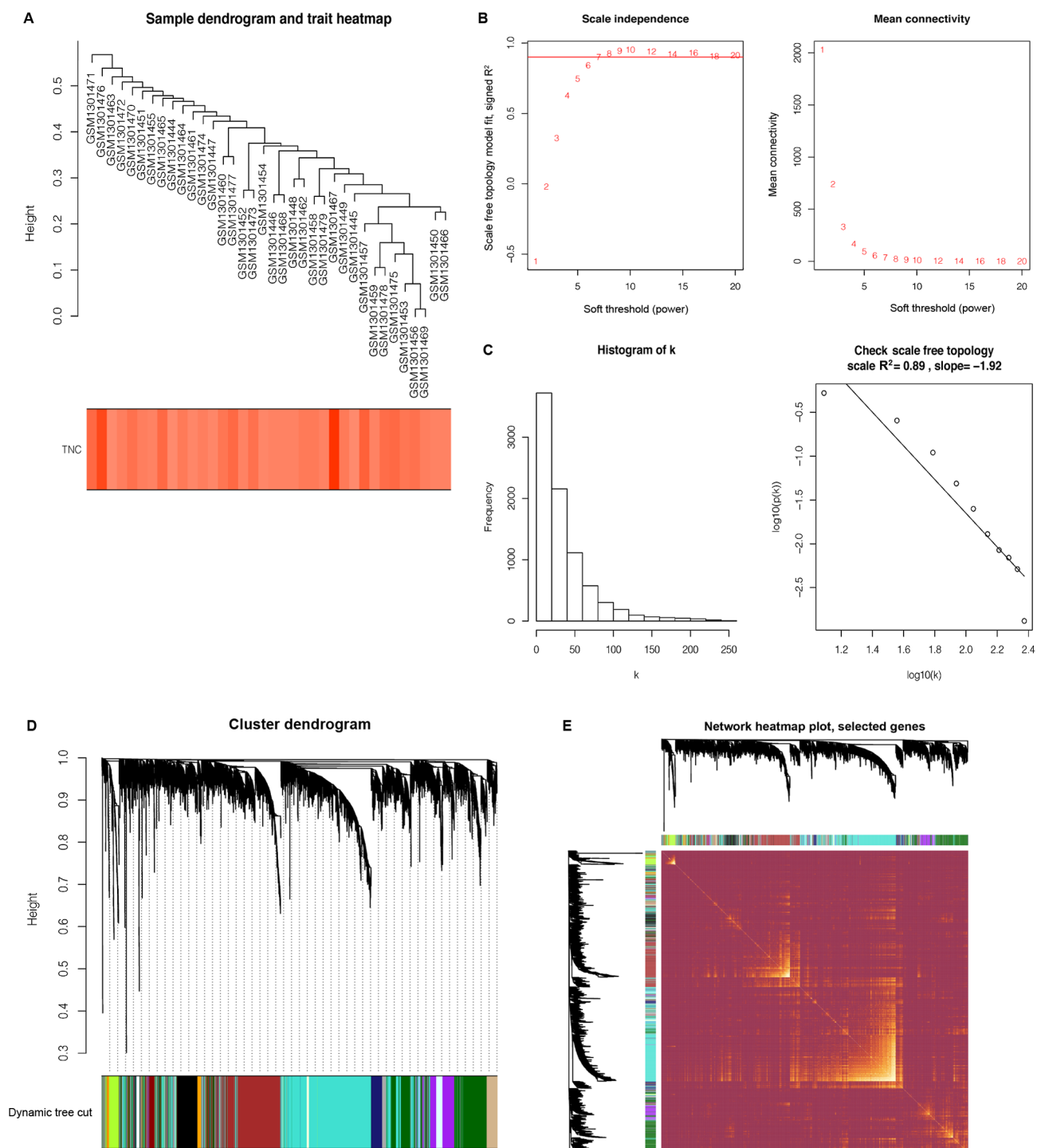
Figure S3. Weighted gene co-expression network analysis. (A) Clustering dendrograms of module eigengenes. Modules below the red line indicate that the correlation was >0.8, and these were merged. (B) Heatmap of the expression volume of the light cyan module and the histogram of the feature vector gene.
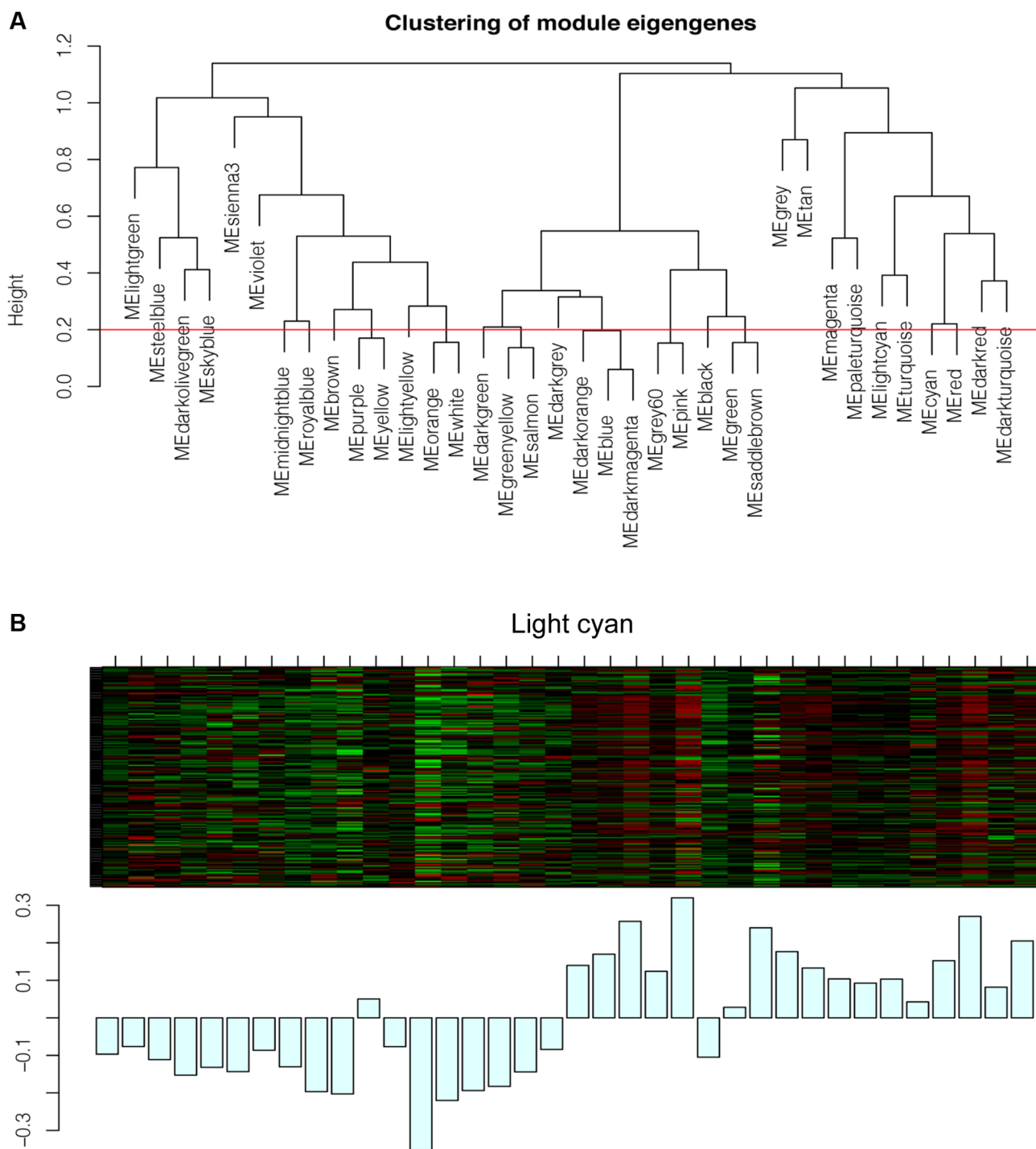
Figure S4. Weighted gene co-expression network analysis. Correlation between intermodular connectivity and the module membership.

Correlation=0.97, P=0.00001